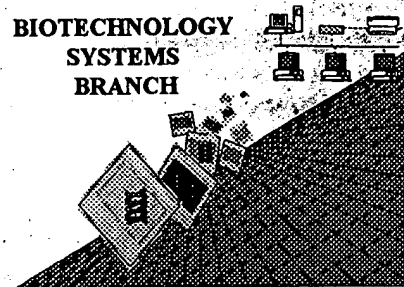W. Moore

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: __09/147,947__

Art Unit / Team No. : __1652__

Date Processed by STIC: __11/15/99__

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/147,947_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
· Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Us of <220>Featur (NEW RULES)
Sequence(s) _____ are missing the <220>Featur and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "C py to Disk" function of PatentIn version 2.0. This causes a corrupted
fil , r sulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file t floppy disk.

W̶ Moore

> **This Raw Listing contains the General Information Section and up to first 5 pages.**

Does Not Comply
Corrected Diskette Needed

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 1    <110> APPLICANT: TSURUOKA, Nobuo
 2          YAMASHIRO, Kyoko
 3          YAMAGUCHI, Nozomi
 4    <120> TITLE OF INVENTION: Novel Serine Protease
 5    <130> FILE REFERENCE: 001560-349
 6    <140> CURRENT APPLICATION NUMBER: US/09/147,947
 7    <141> CURRENT FILING DATE: 1999-03-24
 8    <150> EARLIER APPLICATION NUMBER: PCT/JP98/03324
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41        agcc atg gcg ctc gcc cgc tgc gtg ctg gct gtg att tta ggg gca ctg     289
42             Met Ala Leu Ala Arg Cys Val Leu Ala Val Ile Leu Gly Ala Leu
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50        tcg cgg cgg cca ccc agg acc ccg cgc ttc ccg ctc ccg ctg cgg atc      433
51        Ser Arg Arg Pro Pro Arg Thr Pro Arg Phe Pro Leu Pro Leu Arg Ile
52                        50                  55                  60
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56        acg att cca cgc cgc tgc ggg gca gga gag tcg tgg ggc aat gcc acc      529
57        Thr Ile Pro Arg Arg Cys Gly Ala Gly Glu Ser Trp Gly Asn Ala Thr
58        80                  85                  90                  95
59        aac ctc ggc gtc ccg tgt cta cac tgg gac gag gtg ccg ccc ttc ctg      577
60        Asn Leu Gly Val Pro Cys Leu His Trp Asp Glu Val Pro Pro Phe Leu
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63        Glu Arg Ser Pro Pro Ala Ser Trp Ala Glu Leu Arg Gly Gln Pro His
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65        aac ttc tgc cgg agc ccg gat ggc tcg ggc aga cct tgg tgc ttc tat      673
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68        cgg aat gcc cag ggc aaa gta gac tgg ggc tac tgc gat tgt ggt caa      721
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75        Glu Gly Arg Val Glu Leu Tyr His Ala Gly Gln Trp Gly Thr Ile Cys
76                        180                 185                 190
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87        Leu Ser Ile Glu Gln Cys Pro Lys Ser Ser Trp Gly Glu His Asn Cys
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119        acc gat aag cat gca gct gtg atc tgc cgg cag ctt ggc tat aag ggt      1537
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122        cct gcc aga gca agg act atg gct tat ttt ggg gaa gga aaa ggc ccc      1585
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127                450                 455                 460

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151                    580                   585                   590
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154                    595                   600                   605
155        aga agc gac tat gac att gcc ctg gtt aga ttg caa gga cca ggg gag       2113
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157                    610                   615                   620
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175        705                   710                   715
176        cct gat gag tcc tgg gtt gtg tat ggg gtg act tcc tgg ggg tat gga       2449
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181                    740                   745                   750
182        gta cct tgg ata aaa agt gtc acc agt ctg taacttatgg aaagctcaag        2547
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199                35              40              45
200    Arg Arg Pro Pro Arg Thr Pro Arg Phe Pro Leu Pro Leu Arg Ile Pro
201            50              55              60
202    Ala Ala Gln Arg Pro Gln Val Leu Ser Thr Gly His Thr Pro Pro Thr
203    65              70              75              80
204    Ile Pro Arg Arg Cys Gly Ala Gly Glu Ser Trp Gly Asn Ala Thr Asn
205                85              90              95
206    Leu Gly Val Pro Cys Leu His Trp Asp Glu Val Pro Pro Phe Leu Glu
207                100             105             110
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211        130             135             140
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213    145             150             155             160
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217                180             185             190
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219            195             200             205
220    Leu Ser Gly Ile Ala Lys Ala Trp His Gln Ala His Phe Gly Glu Gly
221        210             215             220
222    Ser Gly Pro Ile Leu Leu Asp Glu Val Arg Cys Thr Gly Asn Glu Leu
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225                245             250             255
226    His Lys Glu Asp Ala Gly Val Ser Cys Val Pro Leu Thr Asp Gly Val
227                260             265             270
228    Ile Arg Leu Ala Gly Gly Lys Ser Thr His Glu Gly Arg Leu Glu Val
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230    Tyr Tyr Lys Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp Thr Glu
231        290             295             300
232    Met Asn Thr Tyr Val Ala Cys Arg Leu Leu Gly Phe Lys Tyr Gly Lys
233    305             310             315             320
234    Gln Ser Ser Val Asn His Phe Asp Gly Ser Asn Arg Pro Ile Trp Leu
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238    Arg Arg Gln Trp Gly Arg His Asp Cys Ser His Arg Glu Asp Val Gly
239                355             360             365
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241        370             375             380
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244    Val Phe Val Asn Gly Gln Trp Gly Thr Ile Cys Asp Asp Gly Trp Thr
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/147,947**

Input Set: **I147947.RAW**

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29	W	"N" or "Xaa" used: Feature required	agcggnccnc cdgartcvcc